

(FILE 'HOME' ENTERED AT 13:42:14 ON 27 FEB 2001)

INDEX 'ADISALERTS, ADISINSIGHT, AGRICOLA, ANABSTR, AQUASCI, BIOBUSINESS, BIOCOMMERCE, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CANCERLIT, CAPLUS, CEABA-VTB, CEN, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DRUGB, DRUGLAUNCH, DRUGMONOG2, DRUGNL, ...' ENTERED AT 13:42:21 ON 27

FEB

2001

SEA (DS4152) (20W)ANGIO? AND (CANCER OR TUMOR OR TUMOUR)

1 FILE CANCERLIT

1 FILE CAPLUS

1 FILE IFIPAT

11 FILE USPATFULL

L1

QUE (DS4152) (20W) ANGIO? AND (CANCER OR TUMOR OR TUMOUR)

FILE 'USPATFULL, CANCERLIT, CAPLUS, IFIPAT' ENTERED AT 13:44:38 ON 27

FEB

2001

L2

14 S (DS4152) (20W)ANGIO? AND (CANCER OR TUMOR OR TUMOUR)

L3

13 DUP REM L2 (1 DUPLICATE REMOVED)

=> d his

(FILE 'HOME' ENTERED AT 13:42:14 ON 27 FEB 2001)

INDEX 'ADISALERTS, ADISINSIGHT, AGRICOLA, ANABSTR, AQUASCI, BIOBUSINESS,
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CAPLUS, CEABA-VTB, CEN, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE,
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13 DUP REM L2 (1 DUPLICATE REMOVED)

WEST[Help](#)[Logout](#)[Interrupt](#)[Main Menu](#)[Search Form](#)[Posting Counts](#)[Show S Numbers](#)[Edit S Numbers](#)[Preferences](#)**Search Results -**

Terms	Documents
15 and example	1

Database:

US Patents Full-Text Database	▲
JPO Abstracts Database	
EPO Abstracts Database	
Derwent World Patents Index	
IBM Technical Disclosure Bulletins	▼

15 and example

Refine Search:

[Clear](#)**Search History**

Today's Date: 2/27/2001

<u>DB Name</u>	<u>Query</u>	<u>Hit Count</u>	<u>Set Name</u>
USPT	15 and example	1	<u>L6</u>
USPT	13 and antibod?	1	<u>L5</u>
USPT	13 and antibody	1	<u>L4</u>
USPT	5912324	1	<u>L3</u>
EPAB	9514714	1	<u>L2</u>
EPAB	9812226	1	<u>L1</u>

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 27, 2001, 08:59:59 ; Search time 15.59 Seconds
(without alignments)
19.740 Million cell updates/sec

Title: US-09-307-223-1

Perfect score: 57
Sequence: 1 CRRETAWAC 9

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 segs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_36.*
1: /SIDSL/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SIDSL/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SIDSL/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SIDSL/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /SIDSL/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /SIDSL/gcgdata/geneseq/geneseq/AA1985.DAT.*
7: /SIDSL/gcgdata/geneseq/geneseq/AA1986.DAT.*
8: /SIDSL/gcgdata/geneseq/geneseq/AA1987.DAT.*
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17: /SIDSL/gcgdata/geneseq/geneseq/AA1996.DAT.*
18: /SIDSL/gcgdata/geneseq/geneseq/AA1997.DAT.*
19: /SIDSL/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SIDSL/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SIDSL/gcgdata/geneseq/geneseq/AA2000.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	100.0	9	16	Alpha5/betal integ
2	57	100.0	9	19	RGD-containing pep
3	57	100.0	9	20	Integrin-binding p
4	57	100.0	9	21	Integrin alpha5bet
5	57	100.0	12	20	Integrin-specific
6	57	100.0	12	20	Integrin-binding p
7	57	100.0	13	16	Integrin-specific
8	57	100.0	13	19	Chimeric adenoviru
9	57	100.0	25	20	Integrin-binding p
10	43	75.4	9	16	Alpha5/betal integ
11	43	75.4	10	16	Alpha5/betal integ
12	40	70.2	9	16	Alpha5/betal integ

13	40	70.2	170	20	Y29195	Amino acid sequenc
14	39	68.4	7	16	R76198	Alpha5/betal integ
15	39	68.4	7	16	R76192	Alpha5/betal integ
16	38	66.7	14	20	Y42754	Wheat amyloplast A
17	38	66.7	14	20	Y39332	ADP glucose transp
18	38	66.7	132	20	Y73857	Human prostate tum
19	37	64.9	9	19	W66171	MSH-receptor subty
20	37	64.9	269	21	Y75616	Neisseria meningit
21	37	64.9	269	21	Y75617	Neisseria meningit
22	36	63.2	203	20	Y04837	Mycobacterium spec
23	36	63.2	241	20	Y41528	Fragment of human
24	36	63.2	506	20	Y04841	Mycobacterium spec
25	35	61.4	188	21	Y76166	Human secreted pro
26	35	61.4	230	20	Y36783	Protein which is s
27	35	61.4	237	20	W88124	Primate DCMPI C-le
28	35	61.4	392	11	R07130	H20B receptor. R
29	35	61.4	392	18	W18668	Polliovirus recepto
30	35	61.4	416	11	R07131	H20A receptor. R
31	35	61.4	417	18	W18669	Polliovirus recepto
32	34	59.6	45	20	Y45281	Human secreted pro
33	34	59.6	134	20	Y73896	Human prostate tum
34	34	59.6	357	14	R33560	Antigen produced b
35	34	59.6	384	20	Y42383	Amino acid sequenc
36	34	59.6	384	21	Y84437	Amino acid sequenc
37	34	59.6	444	21	Y76041	Rat skin cell prot
38	34	59.6	444	21	Y76120	Rat skin cell prot
39	34	59.6	659	20	Y06996	Sequence of C3Vs.
40	33	57.9	9	19	W66174	MSH-receptor subty
41	33	57.9	60	20	W88911	Polypeptide fragme
42	33	57.9	211	20	Y31151	Human XPC protein
43	33	57.9	268	13	R28147	Sugar beet chitina
44	33	57.9	271	21	Y74326	Neisseria gonorrhoe
45	33	57.9	437	20	Y32502	Human parkin gene

ALIGNMENTS

RESULT 1

ID R76196 standard; peptide; 9 AA.

XX R76196;

AC R76196;

DT 24-JAN-1996 (first entry)

XX Alpha5/betal integrin binding peptide #7.

DE High affinity; integrin binding peptide; alpha5/betal; alphav/beta5;

KW alphav/beta3; RGD; stable configuration; wound healing;

KW osteoclast attachment; bone; angiogenesis; metastasis; tumour;

KW smooth muscle cell migration.

XX Synthetic.

OS Synthetic.

XX W09514714-A1.

XX 01-JUN-1995.

XX 22-NOV-1994; 94WO-US13542.

XX 04-AUG-1994; 94US-0286861.

PR 24-NOV-1993; 93US-0158001.

XX (LJOL-) LA JOLLA CANCER RES FOUND.

XX Koivunen E, Ruoslahti E;

XX WPI; 1995-206899/27.

PT High affinity integrin binding peptides - can be used to attach
cells to a substrate, inhibit the attachment of osteoclasts to bone,
promote wound healing, inhibit angiogenesis, metastasis of tumours

and migration of smooth muscle cells

Claim 6; Page 60; 86pp; English.

The sequences given in R76185-200 and R79073-94 are high affinity integrin binding peptides which bind to various integrins. Peptides which bind to alpha5/beta1 integrins contain the motifs given in R76185-86 and peptides which bind to alpha5/beta3 and alpha5/beta3 integrins contain the motif given in R76187. Alpha5/beta5 integrins are also bound by RGD containing peptides. These peptides assume a conformationally stabilised configuration which is due to the formation of a disulphide bond, a peptide bond or a lactam bond. These peptides may be used for isolating the complementary integrin from a sample mixture by contacting them under ionic conditions to allow binding of the integrin to the peptide and then separating the integrin from the peptide. They can be used for attaching cells to a substrate, by binding them to the substrate with the cell. The peptides promote wound healing when applied locally and inhibit the attachment of osteoclasts to bone. They inhibit angiogenesis, metastasis of tumours and migration of smooth muscle cells.

Sequence 9 AA;

Query Match 100.0%; Score 57; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9
| | | | |
DB 1 crretawac 9

RESULT 2

ID W57200 standard; peptide; 9 AA.

AC W57200;

DT 05-AUG-1998 (first entry)

DE RGD-containing peptide SEQ ID NO:18 from WO9812226 Example 9.

XX Fibronectin; superfibronectin; first type III repeat unit; I11;
KW angiogenesis; psoriasis; rheumatoid arthritis; cancer; tumour.

XX Synthetic.

XX WO9812226-A1.

XX 26-MAR-1998.

XX 12-SEP-1997; 97WO-US16344.

XX 20-SEP-1996; 96US-0717169.

XX (BURN-) BURNHAM INST.

XX Pasqualini R, Ruoslahti E;

XX WPI; 1998-217210/19.

XX Inhibition of angiogenesis by superfibronectin - useful for
PT treating, e.g. psoriasis, rheumatoid arthritis and various cancers

XX Example 9; Page 63; 103pp; English.

XX A method has been developed of ameliorating cancer, or inhibiting
CC angiogenesis, in a subject. The method comprises administering a
CC superfibronectin or a superfibronectin-generating compound. The
CC present sequence represents a peptide used in an example of the
CC present invention. The method can be used to treat cancer, ocular
CC neovascularisation, diabetic retinopathy, haemangioma, rheumatoid

CC arthritis, psoriasis, granuloma, and granulation tissue. The cancer
CC treated by the method can comprise a solid tumour, such as a melanoma,
CC osteosarcoma, ovarian, vascular or epithelial cell tumour. When it is in
CC an epithelial cell tumour, it is preferably a colon carcinoma, breast
CC carcinoma, or ovarian carcinoma. When it is a vascular cell tumour, it is
CC selected from haemangiomas, Kaposi's sarcoma, lymphangioma, glomangioma,
CC angiosarcoma, or haemangioendothelioma. The method inhibits or prevents
CC a tumour cell metastasis in a subject especially inhibits the tumour
CC cell migration, attachment, or inhibiting growth of a tumour cell in a
CC subject having a pathology with an angioproliferative component, where
CC the inhibition causes regression of the pathology. The route of
CC administration is intravenous, intramuscular, intradermal, subcutaneous,
CC intracranial, intracerebrospinal, epidural, topical or oral
CC administration.

Sequence 9 AA;

Query Match 100.0%; Score 57; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9
| | | | |
DB 1 crretawac 9

RESULT 3

ID W95413 standard; peptide; 9 AA.

XX W95413;

XX 18-MAR-1999 (first entry)

XX Integrin-binding peptide 7.

XX Integrin; transfection complex; integrin-binding; lipid; immunisation;
KW antisense therapy; enzyme; therapeutic agent; immunogen; cystic fibrosis;
KW cancer; viral infection; human immunodeficiency virus; cardiovascular;
KW restenosis; leukaemia; asthma; glaucoma; cyclic; circular.

XX Synthetic.

XX Key Location/Qualifiers

FT Disulfide-bond 1..9 /note= "disulphide bridge"

XX WO9854347-A1.

XX 03-DEC-1998.

XX 29-MAY-1998; 98WO-GB01577.

XX 29-MAY-1997; 97GB-0011115.

XX (CHIL-) INST CHILD HEALTH.

XX Hart SL;

XX WPI; 1999-045366/04.

XX New integrin-targeting transfection complex including lipid - used
PT to improve transfection efficiency for a very wide range of cells,
PT useful in, e.g. antisense therapy and genetic immunisation

XX Claim 10; Page 50; 70pp; English.

XX The invention relates to an integrin-targeting transfection complex. The
CC complex comprises a nucleic acid, an integrin-binding component, a
CC polycationic nucleic acid-binding component and a lipid. The complexes
CC are used for in vivo or in vitro transfection of cells, specifically:
CC (i) for treatment or prevention of disease (in humans or other animals)

CC caused by defective or deficient genes; (ii) for immunisation; (iii) for
 CC antisense therapy, and (iv) for protein production in host cells, e.g.
 CC of enzymes, therapeutic agents, vaccinating immunogens and diagnostic
 CC antigens. Typical of the diseases that can be treated or prevented are
 CC cystic fibrosis, cancer, viral infection (e.g. human immunodeficiency
 CC virus), cardiovascular disease (e.g. restenosis), leukaemia, asthma and
 CC glaucoma. Incorporation of the lipid into the complex increases
 CC transfection levels from 1-10 percent to over 50 percent. This effect is
 CC observed with all cell types tested including those that are resistant to
 CC transfection by most plasmid vectors. The complexes can carry large
 CC genes, up to 125 kb, e.g. an artificial chromosome. The present sequence
 CC represents a claimed example of an integrin-binding peptide used in the
 CC transfection complexes.

XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 57; DB 20; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRRETAWAC 9
 Db 1 crretawac 9

RESULT 4

ID Y56389 standard; peptide; 9 AA.

AC Y56389;

DT 16-FEB-2000 (first entry)

DE Integrin alpha5beta1 cyclic peptide antagonist.

XX Integrin alpha5beta1; inhibition; antagonist; cyclic; detection;
 KW fibronectin; vitronectin; angiogenesis; cancer; anticancer; diagnosis;
 KW antiporiatic; anti-arthritis; anti-angiogenic; anti-inflammatory;
 KW angogenic diseases; diabetic retinopathy; macular degeneration;
 KW haemangioma; psoriasis; rheumatoid arthritis; osteoarthritis; neoplasm;
 KW carcinoma; sarcoma; mesothelioma; teratocarcinoma; astrocytoma;
 KW glioblastoma; metastasis; Crohn's disease; ulcerative colitis.

XX Synthetic.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Disulfide-bond 1..9

PN W09958139-A2.

PD 18-NOV-1999.

PF 07-MAY-1999; 99WO-US09972.

PR 08-MAY-1998; 98US-0084850.

PA (REGC) UNIV CALIFORNIA.

PI Varner JA;

XX WPI; 2000-038958/03.

XX Reducing or inhibiting angiogenesis in tissue by treatment with an
 PT agent that interferes with binding of alpha5beta1 integrin with its
 PT ligand, e.g. for treating cancer

XX Claim 14; Page 55; 68pp; English.

XX The present invention describes a method for reducing or inhibiting
 CC angiogenesis in a tissue by treating alpha5beta1 integrin (I) in the
 CC tissue with an agent (II) that interferes with specific binding of (I)

CC to its ligand (III), expressed in the tissue. The present sequence
 CC represents a specifically claimed (I) cyclic peptide antagonist, for
 CC use in the method of the invention. (II) are specifically used to treat
 CC (or, when labeled, to diagnose) angiogenic diseases of the eye (diabetic
 CC retinopathy or macular degeneration); skin (haemangioma or psoriasis);
 CC joints (rheumatoid arthritis and osteoarthritis); neoplasms (particularly
 CC carcinoma, e.g. of breast, colon, ovary and prostate; also sarcoma,
 CC mesothelioma, teratocarcinoma, astrocytoma and glioblastoma or
 CC metastatic malignancies); or diseases of bone and intestines (Crohn's
 CC disease or ulcerative colitis).

XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 57; DB 21; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRRETAWAC 9

Db 1 crretawac 9

RESULT 5

ID W95412 standard; peptide; 12 AA.

XX W95412;

AC W95412;

DT 18-MAR-1999 (first entry)

DE Integrin-specific peptide.

XX Integrin; transfection complex; integrin-binding; lipid; immunisation;
 KW antisense therapy, enzyme; therapeutic agent; immunogen; cystic fibrosis;
 KW cancer; viral infection; human immunodeficiency virus; cardiovascular;
 KW restenosis; leukaemia; asthma; glaucoma.

XX Synthetic.

XX W09854347-A1.

PD 03-DEC-1998.

PF 29-MAY-1998; 98WO-GB01577.

PR 29-MAY-1997; 97GB-0011115.

PA (CHIL-) INST CHILD HEALTH.

XX Hart SL;

XX WPI; 1999-045366/04.

XX New integrin-targeting transfection complex including lipid - used
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 PT useful in, e.g. antisense therapy and genetic immunisation

XX Claim 11; Page 50; 70pp; English.

XX The invention relates to an integrin-targeting transfection complex. The
 CC complex comprises a nucleic acid, an integrin-binding component, a
 CC polycationic nucleic acid-binding component and a lipid. The complexes
 CC are used for in vivo or in vitro transfection of cells, specifically:
 CC (i) for treatment or prevention of disease (in humans or other animals)
 CC caused by defective or deficient genes; (ii) for immunisation; (iii) for
 CC antisense therapy, and (iv) for protein production in host cells, e.g.
 CC of enzymes, therapeutic agents, vaccinating immunogens and diagnostic
 CC antigens. Typical of the diseases that can be treated or prevented are
 CC cystic fibrosis, cancer, viral infection (e.g. human immunodeficiency
 CC virus), cardiovascular disease (e.g. restenosis), leukaemia, asthma and
 CC glaucoma. Incorporation of the lipid into the complex increases
 CC transfection levels from 1-10 percent to over 50 percent. This effect is

CC observed with all cell types tested including those that are resistant to
 CC transfection by most plasmid vectors. The complexes can carry large
 CC genes, up to 125 kb, e.g. an artificial chromosome. The present sequence
 CC represents a claimed example of an integrin-binding peptide used in the
 CC transfection complexes.

XX SQ Sequence 12 AA;

Query Match 100.0%; Score 57; DB 20; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.0031;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9
 |||||
 Db 3 crretawac 11

RESULT 6

W95411
 ID W95411 standard; peptide; 12 AA.

XX AC W95411;

XX DT 18-MAR-1999 (first entry)

XX DE Integrin-specific peptide.

XX KW Integrin; transfection complex; integrin-binding; lipid; immunisation;
 KW antisense therapy; enzyme; therapeutic agent; immunogen; cystic fibrosis;
 KW cancer; viral infection; human immunodeficiency virus; cardiovascular;
 KW restenosis; leukaemia; asthma; glaucoma; cyclic; circular.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Disulfide-bond 3..11 /note= "disulphide bridge"

XX PN WO9854347-A1.

XX PD 03-DEC-1998.

XX PF 29-MAY-1998; 98WO-GB01577.

XX PR 29-MAY-1997; 97GB-0011115.

XX PA (CHIL-) INST CHILD HEALTH.

XX PI Hart SL;

XX DR WPI; 1999-045366/04.

XX PT New integrin-targeting transfection complex including lipid - used
 PT to improve transfection efficiency for a very wide range of cells,
 PT useful in, e.g. antisense therapy and genetic immunisation

XX PS Claim 11; Page 50; 70pp; English.

XX CC The invention relates to an integrin-targeting transfection complex. The
 CC complex comprises a nucleic acid, an integrin-binding component, a
 CC polycationic nucleic acid-binding component and a lipid. The complexes
 CC are used for in vivo or in vitro transfection of cells, specifically:
 CC (i) for treatment or prevention of disease (in humans or other animals)
 CC caused by defective or deficient genes; (ii) for immunisation; (iii) for
 CC antisense therapy, and (iv) for protein production in host cells, e.g.
 CC of enzymes, therapeutic agents, vaccinating immunogens and diagnostic
 CC antigens. Typical of the diseases that can be treated or prevented are
 CC cystic fibrosis, cancer, viral infection (e.g. human immunodeficiency
 CC virus), cardiovascular disease (e.g. restenosis), leukaemia, asthma and
 CC glaucoma. Incorporation of the lipid into the complex increases
 CC transfection levels from 1-10 percent to over 50 percent. This effect is
 CC observed with all cell types tested including those that are resistant to

CC transfection by most plasmid vectors. The complexes can carry large
 CC genes, up to 125 kb, e.g. an artificial chromosome. The present sequence
 CC represents a claimed example of an integrin-binding peptide used in the
 CC transfection complexes.

XX SQ Sequence 12 AA;

Query Match 100.0%; Score 57; DB 20; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.0031;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9
 |||||
 Db 3 crretawac 11

RESULT 7

R76190
 ID R76190 standard; peptide; 13 AA.

XX AC R76190;

XX DT 24-JAN-1996 (first entry)

XX DE Integrin binding peptide #2.

XX KW High affinity; integrin binding peptide; alpha5/beta1; alphav/beta5;
 KW alphav/beta3; RGD; stable configuration; wound healing;
 KW osteoclast attachment; bone; angiogenesis; metastasis; tumour;
 KW smooth muscle cell migration.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Disulfide-bond 3..11

XX PN WO9514714-A1.

XX PD 01-JUN-1995.

XX PF 22-NOV-1994; 94WO-US13542.

XX PR 04-AUG-1994; 94US-0286861.

XX PR 24-NOV-1993; 93US-0158001.

XX PA (LJOL-) LA JOLLA CANCER RES FOUND.

XX PI Koivunen E, Ruoslahti E;

XX DR WPI; 1995-206899/27.

XX PT High affinity integrin binding peptides - can be used to attach
 PT cells to a substrate, inhibit the attachment of osteoclasts to bone,
 PT promote wound healing, inhibit angiogenesis, metastasis of tumours
 PT and migration of smooth muscle cells

XX PS Example 1; Page 24; 86pp; English.

XX CC The sequences given in R76185-200 and R79073-94 are high affinity
 CC integrin binding peptides which bind to various integrins. Peptides
 CC which bind to alpha5/beta1 integrins contain the motifs given in
 CC R76185-86 and peptides which bind to alphav/beta5 and alphav/beta3
 CC integrins contain the motif given in R76187. Alphav/beta5 integrins
 CC are also bound by RGD containing peptides. These peptides assume a
 CC conformationally stabilised configuration which is due to the
 CC formation of a disulphide bond, a peptide bond or a lactam bond.
 CC These peptides may be used for isolating the complementary integrin
 CC from a sample mixture by contacting them under ionic conditions to
 CC allow binding of the integrin to the peptide and then separating the
 CC integrin from the peptide. They can be used for attaching cells to
 CC a substrate, by binding them to the substrate with the cell. The
 CC peptides promote wound healing when applied locally and inhibit the

CC attachment of osteoclasts to bone. They inhibit angiogenesis,
CC metastasis of tumours and migration of smooth muscle cells.

QQ Sequence 13 AA;

Query Match 100.0%; Score 57; DB 16; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9
| | | | | | | | |
DB 3 crretawac 11

RESULT 8

W56041
ID W56041 standard; peptide: 13 AA.

XX AC W56041;

XX 29-JUL-1998 (first entry)

XX Chimeric adenovirus fiber protein non-native amino acid sequence 35.

XX Chimeric; adenovirus; fiber protein; binding; targeting; coat protein;
KW constrained peptide motif; gene therapy; cancer; heart disease;
KW autoimmune disorder.

XX Synthetic.

OS Mastadenovirus.

XX W09807865-A1.

XX 26-FEB-1998.

XX 21-AUG-1997; 97WO-US14719.

XX 21-AUG-1996; 96US-0701124.

XX (GENV.) GENVEC INC.

XX Kovessdi I, Roelvink PW, Wickham TJ;

XX WPI; 1998-169169/15.

XX N-PSDB; V28551.

XX Chimeric adenovirus fibre proteins - containing non-native amino
PT acid sequence to provide for binding and entry into cells,
PT especially for gene therapy

PS Claim 7; Page 78; 124pp; English.

XX The present sequence represents a specifically claimed non-native amino
CC acid sequence from a chimeric adenovirus fibre protein (Arp) of the
CC present invention. The non-native amino acid sequence allows the
CC chimeric fibre (or a vector comprising the chimeric fibre) to more
CC efficiently bind to and enter cells. The products can be used for gene
CC therapy, for treating cancer, e.g. melanoma, glioma and lung cancers as
CC well as genetic disorders, e.g. cystic fibrosis, haemophilia and
CC muscular dystrophy as well as pathogenic infections, e.g. HIV,
CC tuberculosis and hepatitis and also for heart disease, to e.g. prevent
CC restenosis following angioplasty or to promote angiogenesis to reperfuse
CC necrotic tissue, and in autoimmune disorders, e.g. Crohn's disease,
CC colitis, rheumatoid arthritis, and Alzheimer's disease.

XX Sequence 13 AA;

Query Match 100.0%; Score 57; DB 19; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9
| | | | | | | | |
DB 3 crretawac 11

RESULT 9

W95416
ID W95416 standard; peptide: 25 AA.

XX AC W95416;

XX 18-MAR-1999 (first entry)

XX Integrin-binding peptide.

XX Integrin; transfection complex; integrin-binding; lipid; immunisation;
KW antisense therapy; enzyme; therapeutic agent; immunogen; cystic fibrosis;
KW cancer; viral infection; human immunodeficiency virus; cardiovascular;
KW restenosis; leukaemia; asthma; glaucoma; cyclic; circular.

XX Synthetic.

XX Key Location/Qualifiers

XX Disulfide-bond 3..11 /note= "disulphide bridge"

XX W09854347-A1.

XX 03-DEC-1998.

XX 29-MAY-1998; 98WO-GB01577.

XX 29-MAY-1997; 97GB-0011115.

XX (CHIL-) INST CHILD HEALTH.

XX Hart SL;

XX WPI; 1999-045366/04.

XX New integrin-targeting transfection complex including lipid - used
PT to improve transfection efficiency for a very wide range of cells,
PT useful in, e.g. antisense therapy and genetic immunisation

PS Claim 12; Page 50; 70pp; English.

XX The invention relates to an integrin-targeting transfection complex. The
CC complex comprises a nucleic acid, an integrin-binding component, a
CC polycationic nucleic acid-binding component and a lipid. The complexes
CC are used for in vivo or in vitro transfection of cells, specifically:
CC (i) for treatment or prevention of disease (in humans or other animals)
CC caused by defective or deficient genes; (ii) for immunisation; (iii) for
CC antisense therapy, and (iv) for protein production in host cells, e.g.
CC of enzymes, therapeutic agents, vaccinating immunogens and diagnostic
CC antigens. Typical of the diseases that can be treated or prevented are
CC cystic fibrosis, cancer, viral infection (e.g. human immunodeficiency
CC virus), cardiovascular disease (e.g. restenosis), leukaemia, asthma and
CC glaucoma. Incorporation of the lipid into the complex increases
CC transfection levels from 1-10 percent to over 50 percent. This effect is
CC observed with all cell types tested including those that are resistant to
CC transfection by most plasmid vectors. The complexes can carry large
CC genes, up to 125 kb, e.g. an artificial chromosome. The present sequence
CC represents a claimed example of an integrin-binding peptide used in the
CC transfection complexes.

XX Sequence 25 AA;

Query Match 100.0%; Score 57; DB 20; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.006;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9


```

Db          3 crretawac 11
|||||
RESULT 10
R76195
ID R76195 standard; peptide; 9 AA.
XX
AC R76195;
XX
DT 24-JAN-1996 (first entry)
XX
DE Alpha5/betal integrin binding peptide #6.
XX
KW High affinity; integrin binding peptide; alpha5/betal; alphav/beta5;
KW alphav/beta3; RGD; stable configuration; wound healing;
KW osteoclast attachment; bone; angiogenesis; metastasis; tumour;
KW smooth muscle cell migration.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 3 /note= "Any amino acid, esp. Arg, Lys, Gly, Phe,
FT Glu, Asp, Ala, Ser or His"
FT
FT Misc-difference 6 /note= "Any amino acid, esp. Ala, Glu, Gln, Gly,
FT Leu Ser or Asn"
FT
FT Misc-difference 8 /note= "Any amino acid, esp. Ala, His, Arg, Gln,
FT Trp, Gly, Met or Ser"
FT
XX WO9514714-A1.
XX
PD 01-JUN-1995.
XX
PF 22-NOV-1994; 94WO-US13542.
XX
PR 04-AUG-1994; 94US-0286861.
PR 24-NOV-1993; 93US-0158001.
XX
PA (LJOL-) LA JOLLA CANCER RES FOUND.
XX
PI Koivunen E, Ruoslahti E;
XX
DR WPI; 1995-206899/27.
XX
PS High affinity integrin binding peptides - can be used to attach
PT cells to a substrate, inhibit the attachment of osteoclasts to bone,
PT promote wound healing, inhibit angiogenesis, metastasis of tumours
PT and migration of smooth muscle cells
XX
Claim 8; Page 60; 86pp; English.
XX
CC The sequences given in R76185-200 and R79073-94 are high affinity
CC integrin binding peptides which bind to various integrins. Peptides
CC which bind to alpha5/betal integrins contain the motifs given in
CC R76185-86 and peptides which bind to alphav/beta5 and alphav/beta3
CC integrins contain the motif given in R76187. Alphav/beta5 integrins
CC are also bound by RGD containing peptides. These peptides assume a
CC conformationally stabilised configuration which is due to the
CC formation of a disulphide bond, a peptide bond or a lactam bond.
CC These peptides may be used for isolating the complementary integrin
CC from a sample mixture by contacting them under ionic conditions to
CC allow binding of the integrin to the peptide and then separating the
CC integrin from the peptide. They can be used for attaching cells to
CC a substrate, by binding them to the substrate with the cell...the
CC peptides promote wound healing when applied locally and inhibit the
CC attachment of osteoclasts to bone. They inhibit angiogenesis,
CC metastasis of tumours and migration of smooth muscle cells.
XX
Sequence 9 AA;

```

```

Query Match 75.4%; Score 43; DB 16; length 9;
Best Local Similarity 66.7%; Pred No. 2.1e+05;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9
Db 1 crxetwxc 9

RESULT 11
R79082
ID R79082 standard; peptide; 10 AA.
XX
AC R79082;
XX
DT 24-JAN-1996 (first entry)
XX
DE Alpha5/betal integrin binding peptide #12.
XX
KW High affinity; integrin binding peptide; alpha5/betal; alphav/beta5;
KW alphav/beta3; RGD; stable configuration; wound healing;
KW osteoclast attachment; bone; angiogenesis; metastasis; tumour;
KW smooth muscle cell migration.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1 /note= "Any amino acid"
FT Misc-difference 4 /note= "Any amino acid"
FT Misc-difference 7 /note= "Any amino acid"
FT Misc-difference 9 /note= "Any amino acid"
FT
XX WO9514714-A1.
XX
PD 01-JUN-1995.
XX
PF 22-NOV-1994; 94WO-US13542.
XX
PR 04-AUG-1994; 94US-0286861.
PR 24-NOV-1993; 93US-0158001.
XX
PA (LJOL-) LA JOLLA CANCER RES FOUND.
XX
PI Koivunen E, Ruoslahti E;
XX
DR WPI; 1995-206899/27.
XX
PS High affinity integrin binding peptides - can be used to attach
PT cells to a substrate, inhibit the attachment of osteoclasts to bone,
PT promote wound healing, inhibit angiogenesis, metastasis of tumours
PT and migration of smooth muscle cells
XX
Example 8; Page 33; 86pp; English.
XX
CC The sequences given in R76185-200 and R79073-94 are high affinity
CC integrin binding peptides which bind to various integrins. Peptides
CC which bind to alpha5/betal integrins contain the motifs given in
CC R76185-86 and peptides which bind to alphav/beta5 and alphav/beta3
CC integrins contain the motif given in R76187. Alphav/beta5 integrins
CC are also bound by RGD containing peptides. These peptides assume a
CC conformationally stabilised configuration which is due to the
CC formation of a disulphide bond, a peptide bond or a lactam bond.
CC These peptides may be used for isolating the complementary integrin
CC from a sample mixture by contacting them under ionic conditions to
CC allow binding of the integrin to the peptide and then separating the
CC integrin from the peptide. They can be used for attaching cells to
CC a substrate, by binding them to the substrate with the cell...the
CC peptides promote wound healing when applied locally and inhibit the
CC attachment of osteoclasts to bone. They inhibit angiogenesis,
CC metastasis of tumours and migration of smooth muscle cells.
XX
Sequence 9 AA;

```

Tue Feb 27 09:01:23 2001

CC attachment of osteoclasts to bone. They inhibit angiogenesis,
 CC metastasis of tumours and migration of smooth muscle cells.
 XX
 XX
 SQ

Sequence 10 AA:

Query Match 75.4%; Score 43; DB 16; Length 10;
 Best Local Similarity 66.7%; Pred. No. 0.41;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9
 II III I
 DB 2 crxtxwxc 10

RESULT 12
 ID R79081 standard; peptide; 9 AA.
 XX
 AC R79081;
 XX
 DT 24-JAN-1996 (first entry)
 XX Alpha5/beta1 integrin binding peptide #11.
 DE High affinity; integrin binding peptide; alpha5/beta1; alphav/beta5;
 XX alphav/beta3; RGD; stable configuration; wound healing;
 KW osteoclast attachment; bone; angiogenesis; metastasis; tumour;
 KW smooth muscle cell migration.
 KW Synthetic.

OS
 XX WO9514714-A1.
 PN
 XX 01-JUN-1995.
 PD

XX 22-NOV-1994; 94WO-US13542.
 PF
 XX 04-AUG-1994; 94US-0286861.
 PR
 XX 24-NOV-1993; 93US-0158001.
 PR

XX (LJOL-) LA JOLLA CANCER RES FOUND.

XX Koivunen E, Ruoslahti E;

XX WPI: 1995-206899/27.

XX High affinity integrin binding peptides - can be used to attach
 PT cells to a substrate, inhibit the attachment of osteoclasts to bone,
 PT promote wound healing, inhibit angiogenesis, metastasis of tumours
 PT and migration of smooth muscle cells

XX Example 8; Page 33; 86pp; English.

XX The sequences given in R76185-200 and R79073-94 are high affinity
 CC integrin binding peptides which bind to various integrins. Peptides
 CC which bind to alpha5/beta1 integrins contain the motifs given in
 CC R76185-86 and peptides which bind to alphav/beta5 and alphav/beta3
 CC integrins contain the motif given in R76187. Alphav/beta5 integrins
 CC are also bound by RGD containing peptides. These peptides assume a
 CC conformationally stabilised configuration which is due to the
 CC formation of a disulphide bond, a peptide bond or a lactam bond.
 CC These peptides may be used for isolating the complementary integrin
 CC from a sample mixture by contacting them under ionic conditions to
 CC allow binding of the integrin to the peptide and then separating the
 CC integrin from the peptide. They can be used for attaching cells to
 CC a substrate, by binding them to the substrate with the cell. The
 CC peptides promote wound healing when applied locally and inhibit the
 CC attachment of osteoclasts to bone. They inhibit angiogenesis,
 CC metastasis of tumours and migration of smooth muscle cells.

XX Sequence 9 AA;

Query Match 70.2%; Score 40; DB 16; Length 9;
 Best Local Similarity 66.7%; Pred. No. 2.1e+05;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9
 II III I
 DB 1 crsetywc 9

RESULT 13
 Y29195
 ID Y29195 standard; Protein; 170 AA.
 XX
 AC Y29195;
 XX
 DT 25-OCT-1999 (first entry)
 XX Amino acid sequence of a virulence factor encoded by ORF26762c.
 DE Human pathogen; virulence polypeptide; virulence factor;
 XX pathogenic infection; Pseudomonas aeruginosa infection.
 KW Pseudomonas aeruginosa.
 XX
 OS WO9927129-A1.
 XX
 PN 03-JUN-1999.
 PD

XX 25-NOV-1998; 98WO-US25247.
 PF
 XX 25-NOV-1997; 97US-0066517.
 PR
 XX (GEHO) GEN HOSPITAL CORP.
 XX Ausubel F, Cao H, Drenkard E, Goodman HM, Mahajan-Miklos S;
 PI Rahme LG, Tan M, Tsongalis J;
 PI WPI: 1999-357851/30.
 XX

XX Virulence factors useful in developing disease treatments
 XX
 XX Disclosure; Fig 4; 228pp; English.
 XX The present sequence represents a Pseudomonas aeruginosa polypeptide
 CC sequence. P. aeruginosa is an opportunistic human pathogen present in
 CC soil water and plants. The specification describes virulence polypeptides
 CC and nucleic acid sequence encoding such polypeptides. These sequences
 CC can be used to identify a compound which is capable of decreasing the
 CC expression of a pathogenic virulence factor. Compounds that inhibit
 CC the expression or activity of virulence factor polypeptides can be
 CC used to treat pathogenic infections, especially where the infection
 CC is a P. aeruginosa infection.
 CC note: the sequences given in the specification were poorly legible, and
 CC in some instances assumptions were made as to the identity of the
 CC residue; it is therefore possible that the sequence given below is
 CC not entirely correct.
 XX

SQ Sequence 170 AA;

Query Match 70.2%; Score 40; DB 20; Length 170;
 Best Local Similarity 87.5%; Pred. No. 15;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RRETAWAC 9
 II III I
 DB 34 rrtawac 41

RESULT 14
 R76198
 ID R76198 standard; peptide; 7 AA.

XX R76198;
 AC
 DT 24-JAN-1996 (first entry)
 XX
 DE Alpha5/betal integrin binding peptide #9.
 XX
 KW High affinity; integrin binding peptide; alpha5/betal; alphav/beta5;
 KW alphav/beta3; RGD; stable configuration; wound healing;
 KW osteoclast attachment; bone; angiogenesis; metastasis; tumour;
 KW smooth muscle cell migration.
 XX
 OS Synthetic.
 XX
 PN WO9514714-A1.
 XX
 PD 01-JUN-1995.
 XX
 PF 22-NOV-1994; 94WO-US13542.
 XX
 PR 04-AUG-1994; 94US-0286861.
 PR 24-NOV-1993; 93US-0158001.
 XX
 PA (LJOL-) LA JOLLA CANCER RES FOUND.
 XX
 PI Koivunen E, Ruoslahti E;
 XX
 DR WPI; 1995-206899/27.
 XX
 PT High affinity integrin binding peptides - can be used to attach
 PT cells to a substrate, inhibit the attachment of osteoclasts to bone,
 PT promote wound healing, inhibit angiogenesis, metastasis of tumours
 PT and migration of smooth muscle cells
 XX
 PS Disclosure; Page 8; 86pp; English.
 XX
 CC The sequences given in R76185-200 and R79073-94 are high affinity
 CC integrin binding peptides which bind to various integrins. Peptides
 CC which bind to alpha5/betal integrins contain the motifs given in
 CC R76185-86 and peptides which bind to alphav/beta5 and alphav/beta3
 CC integrins contain the motif given in R76187. Alphav/beta5 integrins
 CC are also bound by RGD containing peptides. These peptides assume a
 CC conformationally stabilised configuration which is due to the
 CC formation of a disulphide bond, a peptide bond or a lactam bond.
 CC These peptides may be used for isolating the complementary integrin
 CC from a sample mixture by contacting them under ionic conditions to
 CC allow binding of the integrin to the peptide and then separating the
 CC integrin from the peptide. They can be used for attaching cells to
 CC a substrate, by binding them to the substrate with the cell. The
 CC peptides promote wound healing when applied locally and inhibit the
 CC attachment of osteoclasts to bone. They inhibit angiogenesis,
 CC metastasis of tumours and migration of smooth muscle cells.
 XX
 SQ Sequence 7 AA;
 Query Match 68.4%; Score 39; DB 16; Length 7;
 Best Local Similarity 100.0%; Pred. NO. 2.1e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 RRETAWA 8
 |||||
 Db 1 rretawa 7
 RESULT 15
 R76192
 ID R76192 standard; peptide; 7 AA.
 XX
 AC R76192;
 XX
 DT 24-JAN-1996 (first entry)
 XX

DE Alpha5/betal integrin binding peptide #4.
 XX
 KW High affinity; integrin binding peptide; alpha5/betal; alphav/beta5;
 KW alphav/beta3; RGD; stable configuration; wound healing;
 KW osteoclast attachment; bone; angiogenesis; metastasis; tumour;
 KW smooth muscle cell migration.
 XX
 OS Synthetic.
 XX
 PN WO9514714-A1.
 XX
 PD 01-JUN-1995.
 XX
 PF 22-NOV-1994; 94WO-US13542.
 XX
 PR 04-AUG-1994; 94US-0286861.
 PR 24-NOV-1993; 93US-0158001.
 XX
 PA (LJOL-) LA JOLLA CANCER RES FOUND.
 XX
 PI Koivunen E, Ruoslahti E;
 XX
 DR WPI; 1995-206899/27.
 XX
 PT High affinity integrin binding peptides - can be used to attach
 PT cells to a substrate, inhibit the attachment of osteoclasts to bone,
 PT promote wound healing, inhibit angiogenesis, metastasis of tumours
 PT and migration of smooth muscle cells
 XX
 PS Claim 5; Page 60; 86pp; English.
 XX
 CC The sequences given in R76185-200 and R79073-94 are high affinity
 CC integrin binding peptides which bind to various integrins. Peptides
 CC which bind to alpha5/betal integrins contain the motifs given in
 CC R76185-86 and peptides which bind to alphav/beta5 and alphav/beta3
 CC integrins contain the motif given in R76187. Alphav/beta5 integrins
 CC are also bound by RGD containing peptides. These peptides assume a
 CC conformationally stabilised configuration which is due to the
 CC formation of a disulphide bond, a peptide bond or a lactam bond.
 CC These peptides may be used for isolating the complementary integrin
 CC from a sample mixture by contacting them under ionic conditions to
 CC allow binding of the integrin to the peptide and then separating the
 CC integrin from the peptide. They can be used for attaching cells to
 CC a substrate, by binding them to the substrate with the cell. The
 CC peptides promote wound healing when applied locally and inhibit the
 CC attachment of osteoclasts to bone. They inhibit angiogenesis,
 CC metastasis of tumours and migration of smooth muscle cells.
 XX
 SQ Sequence 7 AA;
 Query Match 68.4%; Score 39; DB 16; Length 7;
 Best Local Similarity 100.0%; Pred. NO. 2.1e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 RRETAWA 8
 |||||
 Db 1 rretawa 7
 Search completed: February 27, 2001, 09:00:55
 Job time: 56 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 27, 2001, 09:00:00 ; Search time 42.98 Seconds
(without alignments)
32.075 Million cell updates/sec

Title: US-09-307-223-1

Perfect score: 57

Sequence: 1 CRRETAWAC 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 954730 seqs, 153174147 residues

Total number of hits satisfying chosen parameters: 954730

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pending_Patents_AA:*

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11: /cgn2_6/ptodata/2/paa/US087_COMB.pep.*
12: /cgn2_6/ptodata/2/paa/US088_COMB.pep.*
13: /cgn2_6/ptodata/2/paa/US089_COMB.pep.*
14: /cgn2_6/ptodata/2/paa/US090_COMB.pep.*
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25: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep.*
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29: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	57	100.0	9	16	US-09-228-901-18
3	57	100.0	9	17	US-09-307-223-1
4	57	100.0	9	17	US-09-364-597A-12
5	57	100.0	9	18	US-09-424-656-13

Sequence 6, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 6, Appl
Sequence 6, Appl
Sequence 63, Appl
Sequence 35, Appl
Sequence 16, Appl
Sequence 23046, A
Sequence 11, Appl
Sequence 11, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 18709, A
Sequence 163, App
Sequence 26215, A
Sequence 43165, A
Sequence 25, Appl
Sequence 25, Appl
Sequence 299, App
Sequence 299, App
Sequence 259, App
Sequence 299, App
Sequence 8, Appl
Sequence 8, Appl
Sequence 241, App
Sequence 240, App
Sequence 32565, A
Sequence 3053, A
Sequence 3067, Ap
Sequence 19138, A
Sequence 697, App
Sequence 29287, A
Sequence 20057, A
Sequence 29707, A
Sequence 33, Appl
Sequence 25510, A
Sequence 328, App
Sequence 351, App

ALIGNMENTS

```
RESULT 1
PCT-US94-13542-12
; Sequence 12, Application PC/TUS9413542
; GENERAL INFORMATION:
; APPLICANT: La Jolla Cancer Research Foundation
; TITLE OF INVENTION: Novel Integrin-Binding Peptides
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/13542
; FILING DATE: 22-NOV-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/158,001
; FILING DATE: 24-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Hook, Gregory
```

REGISTRATION NUMBER: 38,701
REFERENCE/DOCKET NUMBER: FP-LA 1220
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: circular
PCT-US94-13542-12

Query Match 100.0%; Score 57; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.2e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9
| | | | | | | | |
DB 1 CRRETAWAC 9

RESULT 2
US-09-228-901-18
; Sequence 18, Application US/09228901
; GENERAL INFORMATION:
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Methods of Inhibiting Angiogenesis and
; TITLE OF INVENTION: Ameliorating Cancer By Using Superfibronectin
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/228,901
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/717,169
; FILING DATE: 20-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 2017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-228-901-18

Query Match 100.0%; Score 57; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.2e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9
| | | | | | | | |

DB 1 CRRETAWAC 9

RESULT 3
US-09-307-223-1
; Sequence 1, Application US/09307223
; GENERAL INFORMATION:
; APPLICANT: VARNER, JUDITH A.
; TITLE OF INVENTION: METHODS FOR DETECTING AND INHIBITING ANGIOGENESIS
; FILE REFERENCE: 6627VARNPALL
; CURRENT APPLICATION NUMBER: US/09/307,223
; CURRENT FILING DATE: 1999-05-07
; EARLIER APPLICATION NUMBER: 60/084,850
; EARLIER FILING DATE: 1998-05-08
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
; OTHER INFORMATION: PEPTIDE
US-09-307-223-1

Query Match 100.0%; Score 57; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.2e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9
| | | | | | | | |
DB 1 CRRETAWAC 9

RESULT 4
US-09-364-597A-12
; Sequence 12, Application US/09364597A
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Koivunen, Erkki
; TITLE OF INVENTION: Novel Integrin-Binding Peptides
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/364,597A
; FILING DATE: 30-JUL-1999
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/158,001
; FILING DATE: 24-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,861
; FILING DATE: 04-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 3419
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (858) 535-9001
; TELEFAX: (858) 535-8949
; INFORMATION FOR SEQ ID NO: 12:

```
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
US-09-364-597A-12

Query Match      100.0%; Score 57; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.2e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9
Db 1 CRRETAWAC 9

RESULT 5
US-09-424-656-13
; Sequence 13, Application US/09424656
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: INTEGRIN-TARGETING VECTORS HAVING
; TITLE OF INVENTION: ENHANCED TRANSFECTION ACTIVITY
; NUMBER OF SEQUENCES: 16
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/424,656
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9711115.7
; FILING DATE: 29-MAY-1997
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
US-09-424-656-13

Query Match      100.0%; Score 57; DB 18; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.2e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9
Db 1 CRRETAWAC 9

RESULT 6
US-60-208-451-6
; Sequence 6, Application US/60208451
; GENERAL INFORMATION:
; APPLICANT: Wickham, Thomas J
; APPLICANT: Kovesdi, Imre
; APPLICANT: Roelvink, Petrus W
; APPLICANT: Einfield, David
; APPLICANT: Brough, Douglas E
; APPLICANT: Lizonova, Alena
; TITLE OF INVENTION: ALTERNATIVELY TARGETED ADENOVIRUS
; FILE REFERENCE: 205046
; CURRENT APPLICATION NUMBER: US/60/208,451
; CURRENT FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT

; ORGANISM: Homo sapiens
US-60-208-451-6

Query Match      100.0%; Score 57; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.2e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9
Db 1 CRRETAWAC 9

RESULT 7
US-09-424-656-11
; Sequence 11, Application US/09424656
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: INTEGRIN-TARGETING VECTORS HAVING
; TITLE OF INVENTION: ENHANCED TRANSFECTION ACTIVITY
; NUMBER OF SEQUENCES: 16
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/424,656
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9711115.7
; FILING DATE: 29-MAY-1997
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
US-09-424-656-11

Query Match      100.0%; Score 57; DB 18; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0083;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9
Db 3 CRRETAWAC 11

RESULT 8
US-09-424-656-12
; Sequence 12, Application US/09424656
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: INTEGRIN-TARGETING VECTORS HAVING
; TITLE OF INVENTION: ENHANCED TRANSFECTION ACTIVITY
; NUMBER OF SEQUENCES: 16
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/424,656
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9711115.7
; FILING DATE: 29-MAY-1997
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
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TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-424-656-12

Query Match 100.0%; Score 57; DB 18; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0083;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRRETAWAC 9
Db 3 CRRETAWAC 11

RESULT 9
PCT-US94-13542-6
; Sequence 6, Application PC/TUS9413542
; GENERAL INFORMATION:
; APPLICANT: La Jolla Cancer Research Foundation
; TITLE OF INVENTION: Novel Integrin-Binding Peptides
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/13542
; FILING DATE: 22-NOV-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/158,001
; FILING DATE: 24-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Hook, Gregory
; REGISTRATION NUMBER: 38,701
; REFERENCE/DOCKET NUMBER: FP-LA 1220
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
PCT-US94-13542-6

Query Match 100.0%; Score 57; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0089;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRRETAWAC 9
Db 3 CRRETAWAC 11

RESULT 10
US-09-364-597A-6
; Sequence 6, Application US/09364597A
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Koivunen, Erkki
; TITLE OF INVENTION: Novel Integrin-Binding Peptides

NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/364,597A
FILING DATE: 30-JUL-1999
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/158,001
FILING DATE: 24-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,861
FILING DATE: 04-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 3419
TELECOMMUNICATION INFORMATION:
TELEPHONE: (858) 535-9001
TELEFAX: (858) 535-8949
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: circular
US-09-364-597A-6

Query Match 100.0%; Score 57; DB 17; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0089;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRRETAWAC 9
Db 3 CRRETAWAC 11

RESULT 11
US-09-406-781-63
; Sequence 63, Application US/09406781
; GENERAL INFORMATION:
; APPLICANT: Kenten, John
; APPLICANT: Roberts, Steven
; TITLE OF INVENTION: CONTROLLING PROTEIN LEVELS IN EUKARYOTIC ORGANISMS
; FILE REFERENCE: 2757-3
; CURRENT APPLICATION NUMBER: US/09/406,781
; CURRENT FILING DATE: 1999-09-28
; EARLIER APPLICATION NUMBER: 60/119,851
; EARLIER FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: binding peptide
US-09-406-781-63

Query Match 100.0%; Score 57; DB 18; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0089;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

us-09-307-223-1.rap

Tue Feb 27 09:01:24 2001

APPLICATION NUMBER: US/09/424,656

FILING DATE:

PRIOR APPLICATION DATA: GB 9711115.7

APPLICATION NUMBER: GB 9711115.7

FILING DATE: 29-MAY-1997

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 25 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: circular

MOLECULE TYPE: peptide

US-09-424-656-16

Query Match 100.0%; Score 57; DB 18; Length 25;

Best Local Similarity 100.0%; Pred. No. 0.016;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9

Db 3 CRRETAWAC 11

RESULT 14

US-09-252-991A-23046

Sequence 23046, Application US/09252991A

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 23046

LENGTH: 196

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-23046

Query Match 78.9%; Score 45; DB 16; Length 196;

Best Local Similarity 77.8%; Pred. No. 8.3;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9

Db 118 CRRETAWAC 126

RESULT 15

PCT-US94-13542-11

Sequence 11, Application PC/TUS9413542

GENERAL INFORMATION:

APPLICANT: La Jolla Cancer Research Foundation

TITLE OF INVENTION: Novel Integrin-Binding Peptides

NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell and Flores

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

1 CRRETAWAC 9

111111111

3 CRRETAWAC 11

RESULT 12

S-09-455-061-35

Sequence 35, Application US/09455061

GENERAL INFORMATION:

APPLICANT: Wickham, Thomas J.

APPLICANT: Roelink, Petrus W.

APPLICANT: Kovesdi, Imre

TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF

TITLE OF INVENTION: CONSTRAINED PEPTIDE MOTIFS

NUMBER OF SEQUENCES: 80

CORRESPONDENCE ADDRESS:

ADDRESSEE: Leydig, Volt & Mayer, Ltd.

STREET: Two Prudential Plaza - 49th Floor

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/455,061

FILING DATE: 06-DEC-1999

PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: US 9-130225

FILING DATE: 06-AUG-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 8-701124

FILING DATE: 21-AUG-1996

ATTORNEY/AGENT INFORMATION:

NAME: Hefner, M. Daniel

REGISTRATION NUMBER: 41,826

REFERENCE/DOCKET NUMBER: 203128

INFORMATION FOR SEQ ID NO: 35:

SEQUENCE CHARACTERISTICS:

LENGTH: 13 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-455-061-35

Query Match 100.0%; Score 57; DB 18; Length 13;

Best Local Similarity 100.0%; Pred. No. 0.0089;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9

111111111

Db 3 CRRETAWAC 11

RESULT 13

US-09-424-656-16

Sequence 16, Application US/09424656

GENERAL INFORMATION:

APPLICANT: INTEGRIN-TARGETING VECTORS HAVING

TITLE OF INVENTION: ENHANCED TRANSFECTION ACTIVITY

NUMBER OF SEQUENCES: 16

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/13542
FILING DATE: 22-NOV-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/158,001
FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Hook, Gregory
REGISTRATION NUMBER: 38,701
REFERENCE/DOCKET NUMBER: FP-LA 1220
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: circular
PCT-US94-13542-11

Query Match 75.4%; Score 43; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. No. 8.2e+05;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CRRETAWAC 9
Db 1 CRXETWXC 9

Search completed: February 27, 2001, 09:02:06
Job time: 126 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 27, 2001, 09:00:00 ; Search time 14.18 seconds
(without alignments)
43.096 Million cell updates/sec

Title: US-09-307-223-1

Perfect score: 57

Sequence: 1 CRRETAWAC 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_66: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	71.9	263	1 S43189	hypothetical prote
2	38	66.7	272	2 T23633	hypothetical prote
3	38	66.7	500	2 T50868	exopolysphatase
4	37	64.9	269	2 G81230	conserved hypothet
5	37	64.9	269	2 D82001	probable integral
6	37	64.9	307	2 D70741	hypothetical prote
7	36	63.2	233	2 H72648	hypothetical prote
8	36	63.2	300	2 A60956	dyein beta heavy
9	36	63.2	323	2 T24372	hypothetical prote
10	36	63.2	334	2 T17213	hypothetical prote
11	36	63.2	465	2 T24419	hypothetical prote
12	36	63.2	535	2 S66148	gene pipsqueak pro
13	36	63.2	2055	2 T00093	hypothetical prote
14	35	61.4	87	2 S36319	T-cell receptor de
15	35	61.4	131	2 S36301	T-cell receptor de
16	35	61.4	136	2 S36320	T-cell receptor de
17	35	61.4	137	2 S36311	T-cell receptor de
18	35	61.4	141	2 S36318	T-cell receptor de
19	35	61.4	142	2 S36316	T-cell receptor de
20	35	61.4	143	2 S36310	T-cell receptor de
21	35	61.4	145	2 S36299	T-cell receptor de
22	35	61.4	265	2 S76808	hypothetical prote
23	35	61.4	284	1 LNRTL	hepatic lectin - r
24	35	61.4	284	2 S29855	asialoglycoprotein
25	35	61.4	347	2 S11223	UDPglucose 4-epime
26	35	61.4	392	1 RWHUPD	poliovirus recepto
27	35	61.4	417	1 RWHUPA	poliovirus recepto
28	35	61.4	417	1 RWHUPA	poliovirus recepto
29	35	61.4	530	2 JC6030	3-oxo-5alpha-ster

30 35 61.4 661 2 T48943
31 35 61.4 1153 2 T21386
32 34 59.6 102 4 JC5161
33 34 59.6 119 2 T17032
34 34 59.6 137 2 I46628
35 34 59.6 139 2 I46630
36 34 59.6 142 2 S36307
37 34 59.6 143 2 S36321
38 34 59.6 144 2 S36322
39 34 59.6 145 2 I46629
40 34 59.6 145 2 I46631
41 34 59.6 149 2 S36317
42 34 59.6 151 2 I46626
43 34 59.6 151 2 T16284
44 34 59.6 155 2 S76397
45 34 59.6 400 2 E71338

hypothetical prote
hypothetical prote
hypothetical orfs
fimbriata-associat
rearranged T-cell
rearranged T-cell
T-cell receptor de
T-cell receptor de
T-cell receptor de
rearranged T-cell
rearranged T-cell
T-cell receptor de
rearranged T-cell
hypothetical prote
hypothetical prote
probable ribose/ga

ALIGNMENTS

RESULT 1
S43189
hypothetical protein - Pseudomonas aeruginosa
C:Species: Pseudomonas aeruginosa
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S43189
R:Strich, U.; Wohlfarth, S.; Winkler, U.K.
submitted to the EMBL Data Library, April 1992
A:Reference number: S43188
A:Accession: S43189
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-263 <STR>
A:Cross-references: EMBL:X65613; NID:g469099; PIDN:CAA46565.1; PID:g469101
C:Superfamily: methanol dehydrogenase regulatory protein

Query Match 71.9%; Score 41; DB 1; Length 263;
Best Local Similarity 66.7%; Pred. No. 3.3;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9
||| |||
Db 240 CRRVAVWRC 248

RESULT 2
T23633
hypothetical protein LLCl.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T23633
R:Matthews, L.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19775
A:Accession: T23633
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-272 <WIL>
A:Cross-references: EMBL:Z82277; PIDN:CAB05250.1; GSPDB:GN00022; CESP:LLC1.2
A:Experimental source: clone LLC1
C:Genetics:
A:Gene: CESP:LLC1.2
A:Map position: 4
A:Introns: 8/1; 81/2; 110/3; 132/1; 172/2; 222/1

Query Match 66.7%; Score 38; DB 2; Length 272;
Best Local Similarity 61.5%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 1; Indels 4; Gaps 1;

QY 1 CRRE----TAWAC 9

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Db 190 CRREAGVATWAC 202
|||||
RESULT 3
T50868
exopolysphatase [imported] - Rubrivivax gelatinosus
C:Species: Rubrivivax gelatinosus
C>Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 18-Aug-2000
C:Accession: T50868
R:Nagashima, K.V.; Igarashi, N.; Harada, J.; Nagashima, S.; Matsuura, K.; Shimada, K.
submitted to the EMBL Data Library, November 1999
A:Description: Determination of Nucleotide Sequences of Rubrivivax gelatinosus Photosyn
A:Reference number: 225270
A:Accession: T50868
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-500 <NAG>
A:Cross-references: EMBL:AB034704; PIDN:BAA94021.1
A:Experimental source: strain IL144
C:Genetics:
A:Gene: ppx
C:Superfamily: exopolysphatase

Query Match 66.7%; Score 38; DB 2; Length 500;
Best Local Similarity 75.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RRETAWAC 9
|||||
Db 360 RRELGNAC 367

RESULT 4
G81230
conserved hypothetical protein NMB0175 [imported] - Neisseria meningitidis (group B stra
C:Species: Neisseria meningitidis
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 31-Mar-2000
C:Accession: G81230
R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Massignani, V.; Pizza, M.;
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: A81000; MUID:20175755
A:Accession: G81230
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-269 <TET>
A:Cross-references: GB:AE002374; GB:AE002098; NID:g7225382; PIDN:AAF40632.1; PID:g722539
A:Experimental source: serogroup B, strain NMD58
C:Genetics:
A:Gene: NMB0175

Query Match 64.9%; Score 37; DB 2; Length 269;
Best Local Similarity 62.5%; Pred. No. 18;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 RRETAWAC 9
|||||
Db 193 RKKTWAC 190

RESULT 5
D82001
probable integral membrane protein NMA0093 [imported] - Neisseria meningitidis (group A
C:Species: Neisseria meningitidis
C>Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-May-2000
C:Accession: D82001
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel

; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandre
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491
A:Reference number: A81775; MUID:2022556
A:Accession: D82001
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-269 <PAR>
A:Cross-references: GB:AL162752; GB:AL157959; NID:g7378778; PIDN:CAB83409.1; PID:g7377
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: NMA0093

Query Match 64.9%; Score 37; DB 2; Length 269;
Best Local Similarity 62.5%; Pred. No. 18;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 RRETAWAC 9
|||||
Db 183 RKKTWAC 190

RESULT 6
D70741
hypothetical protein Rv1357c - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C:Accession: D70741
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd,
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno
A:Reference number: A70500; MUID:98295987
A:Accession: D70741
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-307 <COL>
A:Cross-references: GB:275555; GB:AL123456; NID:g3261608; PIDN:CAA99962.1; PID:e25055
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: Rv1357c

Query Match 64.9%; Score 37; DB 2; Length 307;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9
|||||
Db 5 CORATAFAC 13

RESULT 7
H72648
hypothetical protein AP50622 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C:Accession: H72648
R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Ta
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.
DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero
A:Reference number: A72450; MUID:99310339
A:Accession: H72648
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-233 <KAW>
A:Cross-references: DDBJ:AP000060; NID:g5104188; PIDN:BAW79592.1; PID:d1043378; PID:9
A:Experimental source: strain K1
C:Genetics:

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A:Gene: APE0622

Query Match 63.2%; Score 36; DB 2; Length 233;
Best Local Similarity 55.6%; Pred. No. 24;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9
I: I I I I I
Db 164 CQAPAAWAC 172

RESULT 8
A60956

dynein beta heavy chain, ciliary - sea urchin (Strongylocentrotus purpuratus) (fragment)
C:Species: Strongylocentrotus purpuratus (purple urchin)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 11-Jan-2000
C:Accession: A60956
R:Fortz, K.R.; Asai, D.J.
Cell Motil. Cytoskeleton 16, 33-46, 1990
A:Title: Molecular cloning and expression of sea urchin embryonic ciliary dynein beta he

A:Reference number: A60956; MUID:90284040.

A:Accession: A60956
A:Status: not compared with conceptual translation

A:Molecule type: mRNA
A:Residues: 1-300 <FOL>

C:Superfamily: Escherichia citrate (pro-3S)-lyase alpha chain

Query Match 63.2%; Score 36; DB 2; Length 300;
Best Local Similarity 66.7%; Pred. No. 30;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9
I: I I I I I
Db 4 CQDTRAKAC 12

RESULT 9
T24372

hypothetical protein T02G6.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C:Accession: T24372

R:McLay, K.

submitted to the EMBL Data Library, November 1996

A:Reference number: Z19883

A:Accession: T24372

A:Status: preliminary; translated from GB/EMBL/DBBJ

A:Molecule type: DNA

A:Residues: 1-323 <WIL>

A:Cross-references: EMBL:Z81583; PIDN:CAB04669.1; GSPDB:GN00019; CESP:T02G6.4
A:Experimental source: clone T02G6

C:Genetics:

A:Gene: CESP:T02G6.4

A:Map position: 1

A:Introns: 96/1; 144/2; 177/1; 203/3; 224/2; 237/3; 255/2; 286/1; 312/2

C:Superfamily: Caenorhabditis elegans hypothetical protein T02G6.4

Query Match 63.2%; Score 36; DB 2; Length 323;
Best Local Similarity 44.4%; Pred. No. 32;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9
I: I I I I I
Db 272 CORRSWAC 280

RESULT 10
T17213

hypothetical protein DKFZp434E0335.1 - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T17213

R:Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, September 1999

A:Reference number: Z18723

A:Accession: T17213

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-334 <POU>

A:Cross-references: EMBL:AL117402

A:Experimental source: adult testis; clone DKFZp434E0335

C:Genetics:

A:Note: DKFZp434E0335.1

Query Match 63.2%; Score 36; DB 2; Length 334;
Best Local Similarity 71.4%; Pred. No. 33;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRRETAW 7
I: I I I I I
Db 175 CRDITLM 181

RESULT 11
T24419

hypothetical protein T04A11.10 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jul-2000

C:Accession: T24419

R:Barlow, K.

submitted to the EMBL Data Library, November 1996

A:Reference number: Z19888

A:Accession: T24419

A:Status: preliminary; translated from GB/EMBL/DBBJ

A:Molecule type: DNA

A:Residues: 1-465 <WIL>

A:Cross-references: EMBL:Z83123; PIDN:CAB05613.1; GSPDB:GN00022; CESP:T04A11.10

A:Experimental source: clone T04A11

C:Genetics:

A:Gene: CESP:T04A11.10

A:Map position: 4

A:Introns: 78/3; 148/3; 232/3; 270/2; 368/1

C:Superfamily: Caenorhabditis elegans hypothetical protein C33A12.9b

Query Match 63.2%; Score 36; DB 2; Length 465;
Best Local Similarity 44.4%; Pred. No. 44;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9
I: I I I I I
Db 454 CKRRCSTWC 462

RESULT 12
S66148

gene pipsqueak protein A short form - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jul-2000

C:Accession: S66148

R:Weber, U.; Siegel, V.; Mlodzik, M.

EMBO J. 14, 6247-6257, 1995

A:Title: pipsqueak encodes a novel nuclear protein required downstream of seven-up fo

A:Reference number: S66148; MUID:96134923

A:Accession: S66148

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-535 <WEB>

A:Cross-references: EMBL:X90986; NID:g1149498; PIDN:CAAG2473.1; PID:g1149499

C:Genetics:

A:Gene: pipsqueak

C:Superfamily: POZ domain homology

F:21-123/Domain: POZ domain homology <POZ>

Query Match 63.2%; Score 36; DB 2; Length 535;

Best Local Similarity 55.6%; Pred. No.: 49;

Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9

Db 481 CRTAACWAC 489

RESULT 13

T00093

Hypothetical protein KIAA0467 - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 21-Jul-2000

C:Accession: T00093

R:Seiki, N.; Ohira, M.; Nagase, T.; Ishikawa, K.; Miyajima, D.; Nakajima, N.;

DNA Res. 4; 345-349, 1997

A:Title: Characterization of cDNA clones in size-fractionated cDNA libraries from human

A:Reference number: Z14085; MUID:98116662

A:Accession: T00093

A:Status: preliminary; translated from GB/EMBL/DBBJ

A:Molecule type: mRNA

A:Residues: 1-2055 <SEK>

A:Cross-references: EMBL:AB007936; NID:g3413895; PIDN:BAA32312.1; PID:g3413896

A:Experimental source: brain

C:Genetics:

A:Map position: 1

A:Note: KIAA0467

Query Match

Best Local Similarity 63.2%; Score 36; DB 2; Length 2055;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRRETAW 7

Db 1855 CRDRTLW 1861

RESULT 14

S36319

T-cell receptor delta chain precursor - sheep (fragment)

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999

C:Accession: S36319; S23034

R:Hein, W.R.; Dudler, L.

EMBO J. 12, 715-724, 1993

A:Title: Divergent evolution of T cell repertoires: extensive diversity and development

A:Reference number: S36287; MUID:93178447

A:Accession: S36319

A:Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-87 <HEI>

A:Cross-references: EMBL:Z12991; NID:g2246; PIDN:CAA78335.1; PID:g2247

A:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: T-cell receptor

Query Match

Best Local Similarity 61.4%; Score 35; DB 2; Length 87;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRRETAWA 8

Db 43 CRYETWS 50

RESULT 15

S36301

T-cell receptor delta chain - sheep (fragment)

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999

C:Accession: S36301; S22985

R:Hein, W.R.; Dudler, L.

EMBO J. 12, 715-724, 1993

A:Title: Divergent evolution of T cell repertoires: extensive diversity and developme

A:Reference number: S36287; MUID:93178447

A:Accession: S36301

A:Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-131 <HEI>

A:Cross-references: EMBL:Z12973; NID:g2211; PIDN:CAA78317.1; PID:g2212

A:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: T-cell receptor

Query Match

Best Local Similarity 61.4%; Score 35; DB 2; Length 131;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRRETAWA 8

Db 43 CRYETWS 50

Search completed: February 27, 2001, 09:00:36

Job time: 36 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 27, 2001, 08:59:59 ; Search time 12.5 Seconds
(without alignments)
12.929 Million cell updates/sec

Title: US-09-307-223-1
Perfect score: 57
Sequence: 1 CRRETAWAC 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA:*

- 1: /cgn2.6/ptodata/2/1aa/5A_COMB.pep.*
- 2: /cgn2.6/ptodata/2/1aa/5B_COMB.pep.*
- 3: /cgn2.6/ptodata/2/1aa/6_COMB.pep.*
- 4: /cgn2.6/ptodata/2/1aa/PCPUS_COMB.pep.*
- 5: /cgn2.6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	100.0	9	1	US-08-425-238-6
2	57	100.0	9	2	US-08-717-169-18
3	57	100.0	9	2	US-08-286-861-12
4	57	100.0	13	1	US-08-425-238-3
5	57	100.0	13	2	US-08-701-124-35
6	57	100.0	13	2	US-08-286-861-6
7	57	100.0	13	3	US-09-130-225-35
8	43	75.4	9	2	US-08-286-861-11
9	43	75.4	10	2	US-08-286-861-26
10	40	70.2	9	2	US-08-286-861-25
11	39	68.4	7	1	US-08-425-238-5
12	39	68.4	7	2	US-08-286-861-8
13	39	68.4	9	1	US-08-425-238-10
14	39	68.4	13	1	US-08-425-238-11
15	35	61.4	114	5	5514582-10
16	34	59.6	444	3	US-09-188-930-296
17	34	59.6	552	3	US-08-796-899-28
18	33	57.9	211	2	US-08-708-958-2
19	32	56.1	108	2	US-08-560-398-6
20	32	56.1	114	5	5514582-13
21	32	56.1	114	5	5514582-14
22	32	56.1	255	3	US-08-484-905-110
23	32	56.1	255	3	US-08-481-985B-110
24	32	56.1	255	3	US-08-370-476-110
25	32	56.1	539	5	5198359-4
26	32	56.1	539	5	5449756-4
27	31	54.4	33	3	US-08-651-136C-30
28	31	54.4	222	3	US-08-651-136C-14

29	31	54.4	280	2	US-08-969-106-11	Sequence 11, Appl
30	31	54.4	291	2	US-08-688-342-5	Sequence 5, Appl
31	31	54.4	291	2	US-09-113-788-5	Sequence 5, Appl
32	31	54.4	294	3	US-08-651-136C-24	Sequence 24, Appl
33	31	54.4	374	2	US-08-820-170A-25	Sequence 25, Appl
34	31	54.4	374	3	US-09-055-699-25	Sequence 25, Appl
35	31	54.4	374	3	US-09-273-565-25	Sequence 25, Appl
36	31	54.4	374	4	PCT-US95-06385-2	Sequence 2, Appl
37	31	54.4	487	1	US-08-218-943-2	Sequence 2, Appl
38	31	54.4	527	1	US-08-246-583-2	Sequence 2, Appl
39	31	54.4	538	2	US-08-933-227-5	Sequence 5, Appl
40	31	54.4	673	3	US-09-075-272-5	Sequence 5, Appl
41	31	54.4	1089	1	US-08-180-195-36	Sequence 36, Appl
42	31	54.4	1089	1	US-08-168-917-4	Sequence 4, Appl
43	31	54.4	1089	1	US-08-477-329-36	Sequence 36, Appl
44	31	54.4	1089	2	US-08-475-458-36	Sequence 36, Appl
45	31	54.4	1089	2	US-08-460-510-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-425-238-6
; Sequence 6, Application US/08425238
; Patent No. 5627263
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Koivinen, Erkki
; TITLE OF INVENTION: No. 5627263el Integrin-Binding Peptides
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESS: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,238
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/158,001
FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 9775
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-8949
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-425-238-6

Query Match 100.0%; Score 57; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9
| | | | | | | | |
DB 1 CRRETAWAC 9

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286.861
; FILING DATE: 04-AUG-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/158.001
; FILING DATE: 24-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 9992
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
; US-08-286-861-12

Query Match 100.0%; Score 57; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRRETAWAC 9
Db 1 CRRETAWAC 9

RESULT 4
US-08-425-238-3
; Sequence 3, Application US/08425238
; Patent No. 5627263
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Kivinen, Erkki
; TITLE OF INVENTION: No. 5627263el Integrin-Binding Peptides
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425.238
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/158.001
; FILING DATE: 24-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 9775
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; US-08-717-169-18

Query Match 100.0%; Score 57; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRRETAWAC 9
Db 1 CRRETAWAC 9

RESULT 3
US-08-286-861-12
; Sequence 12, Application US/08286861
; Patent No. 5981478
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Kivinen, Erkki
; TITLE OF INVENTION: No. 5981478el Integrin-Binding Peptides
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; US-08-717-169-18

Query Match 100.0%; Score 57; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRRETAWAC 9
Db 1 CRRETAWAC 9

RESULT 2
US-08-717-169-18
; Sequence 18, Application US/08717169
; Patent No. 5922676
; GENERAL INFORMATION:
; APPLICANT: Pasqualini, Renata
; APPLICANT: Ruoslahti, Erkki
; TITLE OF INVENTION: Methods of Inhibiting Angiogenesis and
; TITLE OF INVENTION: Ameliorating Cancer By Using Superfibronectin
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/717.169
; FILING DATE: 20-SEP-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 2017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-717-169-18

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286.861
; FILING DATE: 04-AUG-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/158.001
; FILING DATE: 24-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 9992
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
; US-08-286-861-12

Query Match 100.0%; Score 57; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRRETAWAC 9
Db 1 CRRETAWAC 9

RESULT 4
US-08-425-238-3
; Sequence 3, Application US/08425238
; Patent No. 5627263
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Kivinen, Erkki
; TITLE OF INVENTION: No. 5627263el Integrin-Binding Peptides
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425.238
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/158.001
; FILING DATE: 24-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 9775
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; US-08-717-169-18

Query Match 100.0%; Score 57; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRRETAWAC 9
Db 1 CRRETAWAC 9

RESULT 3
US-08-286-861-12
; Sequence 12, Application US/08286861
; Patent No. 5981478
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Kivinen, Erkki
; TITLE OF INVENTION: No. 5981478el Integrin-Binding Peptides
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; US-08-717-169-18

Query Match 100.0%; Score 57; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRRETAWAC 9
Db 1 CRRETAWAC 9

RESULT 2
US-08-717-169-18
; Sequence 18, Application US/08717169
; Patent No. 5922676
; GENERAL INFORMATION:
; APPLICANT: Pasqualini, Renata
; APPLICANT: Ruoslahti, Erkki
; TITLE OF INVENTION: Methods of Inhibiting Angiogenesis and
; TITLE OF INVENTION: Ameliorating Cancer By Using Superfibronectin
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/717.169
; FILING DATE: 20-SEP-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 2017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-717-169-18

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/286,861
  FILING DATE: 04-AUG-1994
  CLASSIFICATION: 530
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08/158,001
    FILING DATE: 24-NOV-1993
  ATTORNEY/AGENT INFORMATION:
    NAME: Campbell, Cathryn
    REGISTRATION NUMBER: 31,815
    REFERENCE/DOCKET NUMBER: P-LA 9992
    TELECOMMUNICATION INFORMATION:
      TELEPHONE: (619) 535-9001
      TELEFAX: (619) 535-8949
    INFORMATION FOR SEQ ID NO: 6:
      SEQUENCE CHARACTERISTICS:
        LENGTH: 13 amino acids
        TYPE: amino acid
        TOPOLOGY: circular
US-08-286-861-6

Query Match      100.0%; Score 57; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9
DB 3 CRRETAWAC 11

RESULT 7
US-09-130-225-35
; Sequence 35, Application US/09130225
; Patent No. 6057155
; GENERAL INFORMATION:
; APPLICANT: Wickham, Thomas J.
; APPLICANT: Roelvink, Petrus W.
; APPLICANT: Kovesdi, Imre
; TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF
; TITLE OF INVENTION: CONSTRAINED PEPTIDE MOTIFS
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza - 49th Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/701,124
; FILING DATE: 21-AUG-1996
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-701-124-35

Query Match      100.0%; Score 57; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9
DB 3 CRRETAWAC 11

RESULT 6
US-08-286-861-6
; Sequence 6, Application US/08286861
; Patent No. 5981478
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Koivunen, Erkki
; TITLE OF INVENTION: No. 5981478el Integrin-Binding Peptides
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122

```


Query Match 100.0%; Score 57; DB 3; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.0014;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9
 |||||

Db 3 CRRETAWAC 11

RESULT 8

US-08-286-861-11
 ; Sequence 11, Application US/08286861
 ; Patent No. 5981478
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruoslahti, Erkki
 ; APPLICANT: Koivunen, Erkki
 ; TITLE OF INVENTION: No. 5981478el Integrin-Binding Peptides
 ; NUMBER OF SEQUENCES: 46
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Campbell and Flores
 ; STREET: 4370 La Jolla Village Drive, Suite 700
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 92122

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/286,861
 FILING DATE: 04-AUG-1994
 CLASSIFICATION: 530

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/158,001
 FILING DATE: 24-NOV-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Cathryn
 REGISTRATION NUMBER: 31,815
 REFERENCE/DOCKET NUMBER: P-LA 9992
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-8949
 TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 TYPE: amino acid
 TOPOLOGY: circular

US-08-286-861-11

Query Match 75.4%; Score 43; DB 2; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.3e+05;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9
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Db 1 CRXETXWC 9

RESULT 9

US-08-286-861-26
 ; Sequence 26, Application US/08286861
 ; Patent No. 5981478
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruoslahti, Erkki
 ; APPLICANT: Koivunen, Erkki
 ; TITLE OF INVENTION: No. 5981478el Integrin-Binding Peptides
 ; NUMBER OF SEQUENCES: 46
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Campbell and Flores

STREET: 4370 La Jolla Village Drive, Suite 700
 CITY: San Diego
 STATE: California
 COUNTRY: USA
 ZIP: 92122

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/286,861
 FILING DATE: 04-AUG-1994
 CLASSIFICATION: 530

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/158,001
 FILING DATE: 24-NOV-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Cathryn
 REGISTRATION NUMBER: 31,815
 REFERENCE/DOCKET NUMBER: P-LA 9992

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-9001
 TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 TOPOLOGY: both

US-08-286-861-26

Query Match 75.4%; Score 43; DB 2; Length 10;
 Best Local Similarity 66.7%; Pred. No. 0.19;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9
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Db 2 CRXETXWC 10

RESULT 10

US-08-286-861-25
 ; Sequence 25, Application US/08286861
 ; Patent No. 5981478
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruoslahti, Erkki
 ; APPLICANT: Koivunen, Erkki
 ; TITLE OF INVENTION: No. 5981478el Integrin-Binding Peptides
 ; NUMBER OF SEQUENCES: 46
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Campbell and Flores
 ; STREET: 4370 La Jolla Village Drive, Suite 700
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 92122

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/286,861
 FILING DATE: 04-AUG-1994
 CLASSIFICATION: 530

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/158,001
 FILING DATE: 24-NOV-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Cathryn
 REGISTRATION NUMBER: 31,815
 REFERENCE/DOCKET NUMBER: P-LA 9992

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Query Match          68.4%; Score 39; DB 1: Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels
QY      2 RRETAWA 8
Db      1 RRETAWA 7

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;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/425,238
;; FILING DATE:
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/158,001
;; FILING DATE: 24-NOV-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Campbell, Cathryn A.
;; REGISTRATION NUMBER: 31,815
;; REFERENCE/DOCKET NUMBER: P-LA 9775
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (619) 535-9001
;; TELEFAX: (619) 535-8949
;; INFORMATION FOR SEQ ID NO: 10:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; FEATURE:
;; NAME/KEY: Peptide
;; LOCATION: 1
;; OTHER INFORMATION: /note= "Xaa - an amino acid capable
;; OF FORMING A DISULFIDE BOND."
;;
;; NAME/KEY: Peptide
;; LOCATION: 9
;; OTHER INFORMATION: /note= "Xaa - an amino acid capable
;; OF FORMING A DISULFIDE BOND."
;;
US-08-425-238-10

Query Match 68.4%; Score 39; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRETAWA 8
Db 2 RRETAWA 8

RESULT 14
US-08-425-238-11
;; Sequence 11, Application US/08425238
;; Patent No. 5627263
;; GENERAL INFORMATION:
;; APPLICANT: Ruoslahti, Erkki
;; APPLICANT: Koivinen, Erkki
;; TITLE OF INVENTION: No. 5627263el Integrin-Binding Peptides
;; NUMBER OF SEQUENCES: 12
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Campbell and Flores
;; STREET: 4370 La Jolla Village Drive, Suite 700
;; CITY: San Diego
;; STATE: California
;; COUNTRY: USA
;; ZIP: 92122
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/425,238
;; FILING DATE:
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/158,001
;; FILING DATE: 24-NOV-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Campbell, Cathryn A.
;; REGISTRATION NUMBER: 31,815

;; REFERENCE/DOCKET NUMBER: P-LA 9775
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (619) 535-9001
;; TELEFAX: (619) 535-8949
;; INFORMATION FOR SEQ ID NO: 11:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 13 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; FEATURE:
;; NAME/KEY: Peptide
;; LOCATION: 3
;; OTHER INFORMATION: /note= "Xaa - an amino acid capable
;; OF FORMING A DISULFIDE BOND."
;;
;; NAME/KEY: Peptide
;; LOCATION: 11
;; OTHER INFORMATION: /note= "Xaa - an amino acid capable
;; OF FORMING A DISULFIDE BOND."
;;
US-08-425-238-11

Query Match 68.4%; Score 39; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRETAWA 8
Db 4 RRETAWA 10

RESULT 15
5514582-10
;; Patent No. 5514582
;; APPLICANT: CAPON, DANIEL J.; IASKY, LAURENCE A.
;; TITLE OF INVENTION: RECOMBINANT DNA ENCODING HYBRID
;; IMMUNOGLOBULINS
;; NUMBER OF SEQUENCES: 43
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/185,670
;; FILING DATE: 21-JAN-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 986,931
;; FILING DATE: 08-DEC-1992
;; APPLICATION NUMBER: 808,122
;; FILING DATE: 16-DEC-1991
;; APPLICATION NUMBER: 440,625
;; FILING DATE: 22-NOV-1989
;; APPLICATION NUMBER: 315,015
;; FILING DATE: 23-FEB-1989
;; SEQ ID NO: 10:
;; LENGTH: 114
5514582-10

Query Match 61.4%; Score 35; DB 5; Length 114;
Best Local Similarity 55.6%; Pred. No. 35;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CRRETAWAC 9
Db 106 CRPYRWVC 114

Search completed: February 27, 2001, 09:00:18
Job time: 19 sec

